Please replace the paragraph at page 17, line 34, though page 18, line 6 with the following:

The selection of PCR primers will be made according to the portions of the gene sequence that are to be amplified. For use in PCR detection of *P. carinii*, it is advantageous to choose primer-annealing sites that are highly conserved across many different members of the human-*P. carinii MSG* gene family. For instance, it is advantageous to choose primer sites from within the regions of human-*P. carinii* sequence displaying greater than 63% sequence identity across the disclosed family members, *e.g.*, that portion of the gene encoding the conserved carboxy-terminal region of the protein. The highly conserved carboxy-terminal regions of the disclosed genes are as follows: residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

In the Claims:

Please amend the claims to read as follows:

1. (reiterated) A method of detecting the presence of *Pneumocystis carinii* in a biological specimen, comprising:

amplifying a highly conserved region within a human-*P. carinii* nucleic acid sequence, if such sequence is present in the sample, using two or more oligonucleotide primers derived from human-*P. carinii* MSG protein encoding sequence; and

determining whether an amplified sequence is present.

2. (reiterated) The method according to claim 1, wherein amplification of the human-*P. carinii* nucleic acid sequence is by polymerase chain reaction.

3. **(amended)** The method of claim 1, wherein the human-*P. carinii* nucleic acid sequence is a highly conserved region within an MSG-protein encoding sequence, wherein the highly conserved region has at least 79% sequence identity with residues 2821-3072 of *HMSG35* (SEQ ID NO: 13).

4. (**amended**) The method of claim 3, wherein the highly conserved region comprises a sequence selected from the group consisting of: residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

5. (**amended**) The method of claim 1, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides from a sequence chosen from the group consisting of: residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15) and nucleic acid sequences having at least 91% sequence homology with residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

6. (**amended**) The method of claim 5, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides from a nucleic acid sequence having at least 90% sequence homology with residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

7. (**amended**) The method of claim 5, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides from a nucleic acid sequence having at least 95% sequence homology with residues 2894-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14*

(SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2887-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

8. (reiterated) The method of claim 5, wherein the oligonucleotide primers are chosen from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 23, and SEQ ID NO: 24.

9. (reiterated) The method of claim 5, wherein the pair of oligonucleotide primers consist of one upstream primer and one downstream primer.

10. (reiterated) The method of claim 9, wherein:

the upstream primer is chosen from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 23; and

the downstream primer is chosen from the group consisting of: SEQ ID NO: 20 and SEQ ID NO: 24.

11. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 17.

12. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 18.

13. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 19.

14. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 20.

15. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 23.

16. (reiterated) The method of claim 8, wherein one of the oligonucleotide primers comprises SEQ ID NO: 24.

17. (reiterated) The method of claim 1, wherein the biological specimen is from the oropharyngeal tract.

18. (reiterated) The method of claim 1, wherein the biological specimen is from blood.

19. (reiterated) The method of claim 1, wherein the step of determining whether an amplified sequence is present comprises one or more of:

(a) electrophoresis and staining of the amplified sequence; or

(b) hybridization to a labeled probe of the amplified sequence.

20. (reiterated) The method of claim 19, wherein the amplified sequence is detected by hybridization to a labeled probe.

21. (reiterated) The method of claim 22, wherein the probe comprises a detectable non-isotopic label chosen from the group consisting of:

a fluorescent molecule;

a chemiluminescent molecule;

an enzyme;

a co-factor;

an enzyme substrate; and

a hapten.

22. (reiterated) The method of claim 21, wherein the labeled probe comprises a nucleic acid sequence according to SEQ ID NO: 19.

23. (reiterated) A method of detecting the presence of *Pneumocystis carinii* in a biological specimen, comprising: